

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: TANZI, RUDOLPH
WASCO, WILMA
- (ii) TITLE OF INVENTION: Genetic Alterations Related To Familial
Alzheimer's Disease
- (iii) NUMBER OF SEQUENCES: 32
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
 - (B) STREET: 1100 NEW YORK AVENUE, SUITE 600
 - (C) CITY: WASHINGTON
 - (D) STATE: DC
 - (E) COUNTRY: USA
 - (F) ZIP: 20005-3934
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: To be assigned
 - (B) FILING DATE: Herewith
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/706,344
 - (B) FILING DATE: 30-AUG-1996
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 60/003,054
 - (B) FILING DATE: 31-AUG-1995
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: KIM, JUDITH U.
 - (B) REGISTRATION NUMBER: 40,679
 - (C) REFERENCE/DOCKET NUMBER: 0609.4180002
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 202-371-2600
 - (B) TELEFAX: 202-371-2540

(2) INFORMATION FOR SEQ ID NO: 1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2765 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 249..1649

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

TTGGGACAGCG AGCTCCGGGG TCCGCGGTTT CACATCGGAA ACAAACAGC GGCTGGTCTG	60
GAAGGAACCT GAGTACGAG CCGCGGCGGC AGCGGGCGCG CGGGAAGCG TATACCTAAT	120
CTGGGAGCCT GCAAGTGACA ACAGCCTTTC CGGTCCTTAG ACAGCTTGCG CTGGAGGAGA	180
ACACATGAAA GAAAGAACCT CAAGAGGCTT TGTTTTCTGT GAAACAGTAT TTCTATACAG	240
TTGCTCCA ATG ACA GAG TTA CCT GCA CCG TTG TCC TAC TTC CAG AAT GCA Met Thr Glu Leu Pro Ala Pro Leu Ser Tyr Phe Gln Asn Ala	290
CAG ATG TCT GAG GAC AAC CAC CTG AGC AAT ACT GTA CGT AGC CAG AAT Gln Met Ser Glu Asp Asn His Leu Ser Asn Thr Val Arg Ser Gln Asn	338
GAC AAT AGA GAA CGG CAG GAG CAC AAC GAC AGA CGG AGC CTT GGC CAC Asp Asn Arg Glu Arg Gln Glu His Asn Asp Arg Arg Ser Leu Gly His	386
CCT GAG CCA TTA TCT AAT GGA CGA CCC CAG GGT AAC TCC CGG CAG GTG Pro Glu Pro Leu Ser Asn Gly Arg Pro Gln Gly Asn Ser Arg Gln Val	434
GTG GAG CAA GAT GAG GAA GAA GAT GAG GAG CTG ACA TTG AAA TAT GGC Val Glu Gln Asp Glu Glu Glu Asp Glu Glu Leu Thr Leu Lys Tyr Gly	482
GCC AAG CAT GTG ATC ATG CTC TTT GTC CCT GTG ACT CTC TGC ATG GTG Ala Lys His Val Ile Met Leu Phe Val Pro Val Thr Leu Cys Met Val	530
GTG GTC GTG GCT ACC ATT AAG TCA GTC AGC TTT TAT ACC CGG AAG GAT Val Val Val Ala Thr Ile Lys Ser Val Ser Phe Tyr Thr Arg Lys Asp	578
GGG CAG CTA ATC TAT ACC CCA TTC ACA GAA GAT ACC GAG ACT GTG GGC Gly Gln Leu Ile Tyr Thr Pro Phe Thr Glu Asp Thr Glu Thr Val Gly	626
CAG AGA GCC CTG CAC TCA ATT CTG AAT GCT GCC ATC ATG ATC AGT GTC Gln Arg Ala Leu His Ser Ile Leu Asn Ala Ala Ile Met Ile Ser Val	674
ATT GTT GTC ATG ACT ATC CTC CTG GTG GTT CTG TAT AAA TAC AGG TGC Ile Val Val Met Thr Ile Leu Leu Val Val Leu Tyr Lys Tyr Arg Cys	722
TAT AAG GTC ATC CAT GCC TGG CTT ATT ATA TCA TCT CTA TTG TTG CTG Tyr Lys Val Ile His Ala Trp Leu Ile Ile Ser Ser Leu Leu Leu Leu	770
TTC TTT TTT TCA TTC ATT TAC TTG GGG GAA GTG TTT AAA ACC TAT AAC Phe Phe Phe Ser Phe Ile Tyr Leu Gly Glu Val Phe Lys Thr Tyr Asn	818
GTT GCT GTG GAC TAC ATT ACT GTT GCA CTC CTG ATC TGG AAT TTT GGT Val Ala Val Asp Tyr Ile Thr Val Ala Leu Leu Ile Trp Asn Phe Gly	866

GTG GTG GGA ATG ATT TCC ATT CAC TGG AAA GGT CCA CTT CGA CTC CAG Val Val Gly Met Ile Ser Ile His Trp Lys Gly Pro Leu Arg Leu Gln 210 215 220	914
CAG GCA TAT CTC ATT ATG ATT AGT GCC CTC ATG GCC CTG GTG TTT ATC Gln Ala Tyr Leu Ile Met Ile Ser Ala Leu Met Ala Leu Val Phe Ile 225 230 235	962
AAG TAC CTC CCT GAA TGG ACT GCG TGG CTC ATC TTG GCT GTG ATT TCA Lys Tyr Leu Pro Glu Trp Thr Ala Trp Leu Ile Leu Ala Val Ile Ser 240 245 250	1010
GTA TAT GAT TTA GTG GCT GTT TTG TGT CCG AAA GGT CCA CTT CGT ATG Val Tyr Asp Leu Val Ala Val Leu Cys Pro Lys Gly Pro Leu Arg Met 255 260 265 270	1058
CTG GTT GAA ACA GCT CAG GAG AGA AAT GAA ACG CTT TTT CCA GCT CTC Leu Val Glu Thr Ala Gln Glu Arg Asn Glu Thr Leu Phe Pro Ala Leu 275 280 285	1106
ATT TAC TCC TCA ACA ATG GTG TGG TTG GTG AAT ATG GCA GAA GGA GAC Ile Tyr Ser Ser Thr Met Val Trp Leu Val Asn Met Ala Glu Gly Asp 290 295 300	1154
CCG GAA GCT CAA AGG AGA GTA TCC AAA AAT TCC AAG CAT AAT GCA GAA Pro Glu Ala Gln Arg Arg Val Ser Lys Asn Ser Lys His Asn Ala Glu 305 310 315	1202
AGC ACA GAA AGG GAG TCA CAA GAC ACT GTT GCA GAG AAT GAT GAT GGC Ser Thr Glu Arg Glu Ser Gln Asp Thr Val Ala Glu Asn Asp Asp Gly 320 325 330	1250
GGG TTC AGT GAG GAA TGG GAA GCC CAG AGG GAC AGT CAT CTA GGG CCT Gly Phe Ser Glu Glu Trp Glu Ala Gln Arg Asp Ser His Leu Gly Pro 335 340 345 350	1298
CAT CGC TCT ACA CCT GAG TCA CGA GCT GCT GTC CAG GAA CTT TCC AGC His Arg Ser Thr Pro Glu Ser Arg Ala Ala Val Gln Glu Leu Ser Ser 355 360 365	1346
AGT ATC CTC GCT GGT GAA GAC CCA GAG GAA AGG GGA CTA AAA CTT GGA Ser Ile Leu Ala Gly Glu Asp Pro Glu Glu Arg Gly Val Lys Leu Gly 370 375 380	1394
TTG GGA GAT TTC ATT TTC TAC AGT GTT CTG GTT GGT AAA GCC TCA GCA Leu Gly Asp Phe Ile Phe Tyr Ser Val Leu Val Gly Lys Ala Ser Ala 385 390 395	1442
ACA GCC AGT GGA GAC TGG AAC ACA ACC ATA GCC TGT TTC GTA GCC ATA Thr Ala Ser Gly Asp Trp Asn Thr Thr Thr Ile Ala Cys Phe Val Ala Ile 400 405 410	1490
TTA ATT GGT TTG TGC CTT ACA TTA TTA CTC CTT GCC ATT TTC AAG AAA Leu Ile Gly Leu Cys Leu Thr Leu Leu Leu Ala Ile Phe Lys Lys 415 420 425 430	1538
GCA TTG CCA GCT CTT CCA ATC TCC ATC ACC TTT GGG CTT GTT TTC TAC Ala Leu Pro Ala Leu Pro Ile Ser Ile Thr Phe Gly Leu Val Phe Tyr 435 440 445	1586
TTT GCC ACA GAT TAT CTT GTA CAG CCT TTT ATG GAC CAA TTA GCA TTC Phe Ala Thr Asp Tyr Leu Val Gln Pro Phe Met Asp Gln Leu Ala Phe 450 455 460	1634

450	455	460	
CAT CAA TTT TAT ATC TAGCATATTT	GCGGTTAGAA TCCCATGGAT GTTCTCTCTT		1689
His Gln Phe Tyr Ile			
465			
TGACTATAAC CAAATCTGGG GAGGACAAAG	GTGATTTTCC TGTGTCCACA TCTAACAAAG		1749
TCAAGATTCC CGGCTGGACT TTTGCAGCTT	CCTTCCAAGT CTTCCTGACC ACCTTGCACT		1809
ATTGGAGCTTT GGAAGGAGGT GCCTATAGAA	AACGATTTTG AACATACTTC ATCGCAGTGG		1869
ACTGTGTCCC TCGGTGCAGA AACTACCAGA	TTTGAGGGAC GAGGTCAAGG AGATATGATA		1929
GGCCCGGAAG TTGCTGTGCC CCATCAGCAG	CTTGACGCGT GGTCACAGGA CGATTTCCT		1989
GACACTGCGA ACTCTCAGGA CTACCGGTTA	CAAAGAGGTT AGGTGAAGTG GTTTAAACCA		2049
AACGGAACCT TTCATCTTAA ACTACACGTT	GAAAATCAAC CCAATAATTC TGTATTAAC		2109
GAATCTGAA CTTTTCAGGA GGTACTGTGA	GGAAGAGCAG GCACCAGCAG CAGAATGGGG		2169
AATGGAGAGG TGGGCAGGGG TTCCAGCTTC	CCTTTGATT TTTGCTGCAG ACTCATCCTT		2229
TTTAAATGAG ACTTGTTTTC CCCTCTCTTT	GAGTCAAGTC AAATATGTAG ATTGCCTTTG		2289
GCAATCTCTT TTCTCAAGCA CTGACACTCA	TTACCGTCTG TGATTGCCAT TTCTTCCCAA		2349
GGCCAGTCTG AACCTGAGGT TGCTTTATCC	TAAAAGTTTT AACCTCAGGT TCCAAATTC		2409
GTAAATTTTG GAAACAGTAC AGCTATTTCT	CATCAATTCT CTATCATGTT GAAGTCAAAT		2469
TTGGATTTTC CACCAAATTC TGAATTTGTA	GACATACTTG TACGCTCACT TGCCCCAGA		2529
TGCTCTCTCT GTCCTCATT TTTCTCTCCA	CACAAGCAGT CTTTTTCTAC AGCCAGTAAG		2589
GCAGCTCTGT CRTGGTAGCA GATGGTCCCA	TTATTCTAGG GTCTTACTCT TGTATGATG		2649
AAAAGAATGT GITATGAATC GGTGCTGTCA	GCCCTGCTGT CAGACCTTCT TCCACAGCAA		2709
ATGAGATGTA TGCCCAAAGC GGTAGAATTA	AAGAAGAGTA AAATGGCTGT TGAAGC		2765

(2) INFORMATION FOR SEQ ID NO: 2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 467 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met	Thr	Glu	Leu	Pro	Ala	Pro	Leu	Ser	Tyr	Phe	Gln	Asn	Ala	Gln	Met
1				5					10					15	
Ser	Glu	Asp	Asn	His	Leu	Ser	Asn	Thr	Val	Arg	Ser	Gln	Asn	Asp	Asn
			20					25					30		
Arg	Glu	Arg	Gln	Glu	His	Asn	Asp	Arg	Arg	Ser	Leu	Gly	His	Pro	Glu
		35					40					45			

Pro Leu Ser Asn Gly Arg Pro Gln Gly Asn Ser Arg Gln Val Val Glu
50 55 60

Gln Asp Glu Glu Glu Asp Glu Glu Leu Thr Leu Lys Tyr Gly Ala Lys
65 70 75 80

His Val Ile Met Leu Phe Val Pro Val Thr Leu Cys Met Val Val Val
85 90 95

Val Ala Thr Ile Lys Ser Val Ser Phe Tyr Thr Arg Lys Asp Gly Gln
100 105 110

Leu Ile Tyr Thr Pro Phe Thr Glu Asp Thr Glu Thr Val Gly Gln Arg
115 120 125

Ala Leu His Ser Ile Leu Asn Ala Ala Ile Met Ile Ser Val Ile Val
130 135 140

Val Met Thr Ile Leu Leu Val Val Leu Tyr Lys Tyr Arg Cys Tyr Lys
145 150 155 160

Val Ile His Ala Trp Leu Ile Ile Ser Ser Leu Leu Leu Phe Phe
165 170 175

Phe Ser Phe Ile Tyr Leu Gly Glu Val Phe Lys Thr Tyr Asn Val Ala
180 185 190

Val Asp Tyr Ile Thr Val Ala Leu Leu Ile Trp Asn Phe Gly Val Val
195 200 205

Gly Met Ile Ser Ile His Trp Lys Gly Pro Leu Arg Leu Gln Gln Ala
210 215 220

Tyr Leu Ile Met Ile Ser Ala Leu Met Ala Leu Val Phe Ile Lys Tyr
225 230 235 240

Leu Pro Glu Trp Thr Ala Trp Leu Ile Leu Ala Val Ile Ser Val Tyr
245 250 255

Asp Leu Val Ala Val Leu Cys Pro Lys Gly Pro Leu Arg Met Leu Val
260 265 270

Glu Thr Ala Gln Glu Arg Asn Glu Thr Leu Phe Pro Ala Leu Ile Tyr
275 280 285

Ser Ser Thr Met Val Trp Leu Val Asn Met Ala Glu Gly Asp Pro Glu
290 295 300

Ala Gln Arg Arg Val Ser Lys Asn Ser Lys His Asn Ala Glu Ser Thr
305 310 315 320

Glu Arg Glu Ser Gln Asp Thr Val Ala Glu Asn Asp Asp Gly Gly Phe
325 330 335

Ser Glu Glu Trp Glu Glu Ala Gln Arg Asp Ser His Leu Gly Pro His Arg
340 345 350

Ser Thr Pro Glu Ser Arg Ala Ala Val Gln Glu Leu Ser Ser Ser Ile
355 360 365

Leu Ala Gly Glu Asp Pro Glu Glu Arg Gly Val Lys Leu Gly Leu Gly
370 375 380

Asp Phe Ile Phe Tyr Ser Val Leu Val Gly Lys Ala Ser Ala Thr Ala
385 390 395 400

Ser Gly Asp Trp Asn Thr Thr Ile Ala Cys Phe Val Ala Ile Leu Ile
405 410 415

Gly Leu Cys Leu Thr Leu Leu Leu Ala Ile Phe Lys Lys Ala Leu
420 425 430

Pro Ala Leu Pro Ile Ser Ile Thr Phe Gly Leu Val Phe Tyr Phe Ala
435 440 445

Thr Asp Tyr Leu Val Gln Pro Phe Met Asp Gln Leu Ala Phe His Gln
450 455 460

Phe Tyr Ile
465

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2765 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 249..1649

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

TGGGACAGGC AGCTCCGGGG TCCGGGGTTT CACATCGGAA ACAAACAGC GGCTGGTCTG	60
GAAGGAACCT GAGCTACGAG CCGCGGCGGC AGCGGGGCGG CGGGGAAGCG TATACCTAAT	120
CTGGGAGCCT GCAAGTGACA ACAGCCTTTG CGGTCCTTAG ACAGCTTGGC CTGGAGGAGA	180
ACACATGAAA GAAAGAACCT CAAGAGGCTT TGTTTCTGT GAAACAGTAT TCTATACAG	240
TTGCTCCA ATG ACA GAG TTA CCT GCA CCG TTG TCC TAC TTC CAG AAT GCA	290
Met Thr Glu Leu Pro Ala Pro Leu Ser Tyr Phe Gln Asn Ala	
1 5 10	
CAG ATG TCT GAG GAC AAC CAC CTG AGC AAT ACT GTA CGT AGC CAG AAT	338
Gln Met Ser Glu Asp Asn His Leu Ser Asn Thr Val Arg Ser Gln Asn	
15 20 25 30	
GAC AAT AGA GAA CGG CAG GAG CAC AAC GAC AGA CGG AGC CTT GGC CAC	386
Asp Asn Arg Glu Arg Gln Glu His Asn Asp Arg Arg Ser Leu Gly His	
35 40 45	
CCT GAG CCA TTA TCT AAT GGA CGA CCC CAG GGT AAC TCC CGG CAG GTG	434
Pro Glu Pro Leu Ser Asn Gly Arg Pro Gln Gly Asn Ser Arg Gln Val	
50 55 60	
GTG GAG CAA GAT GAG GAA GAA GAT GAG GAG CTG ACA TTG AAA TAT GGC	482
Val Glu Gln Asp Glu Glu Glu Asp Glu Glu Leu Thr Leu Lys Tyr Gly	

65	70	75	
GCC AAG CAT GTG ATC ATG CTC TTT GTC CCT GTG ACT CTC TGC ATG GTG Ala Lys His Val Ile Met Leu Phe Val Pro Val Thr Leu Cys Met Val	530		
80	85	90	
GTG GTC GTG GCT ACC ATT AAG TCA GTC AGC TTT TAT ACC CGG AAG GAT Val Val Val Ala Thr Ile Lys Ser Val Ser Phe Tyr Thr Arg Lys Asp	578		
95	100	105	110
GGG CAG CTA ATC TAT ACC CCA TTC ACA GAA GAT ACC GAG ACT GTG GGC Gly Gln Leu Ile Tyr Thr Pro Phe Thr Glu Asp Thr Glu Thr Val Gly	626		
115	120	125	
CAG AGA GCC CTG CAC TCA ATT CTG AAT GCT GCC ATC ATG ATC AGT GTC Gln Arg Ala Leu His Ser Ile Leu Asn Ala Ala Ile Met Ile Ser Val	674		
130	135	140	
ATT GTT GTC ATG ACT ATC CTC CTG GTG GTT CTG TAT AAA TAC AGG TGC Ile Val Val Met Thr Ile Leu Val Val Leu Tyr Lys Tyr Arg Cys	722		
145	150	155	
TAT AAG GTC ATC CAT GCC TGG CTT ATT ATA TCA TCT CTA TTG TTG CTG Tyr Lys Val Ile His Ala Trp Leu Ile Ile Ser Ser Leu Leu Leu Leu	770		
160	165	170	
TTC TTT TTT TCA TTC ATT TAC TTG GGG GAA GTG TTT AAA ACC TAT AAC Phe Phe Phe Ser Phe Ile Tyr Leu Gly Glu Val Phe Lys Thr Tyr Asn	818		
175	180	185	190
GTT GCT GTG GAC TAC ATT ACT GTT GCA CTC CTG ATC TGG AAT TTT GGT Val Ala Val Asp Tyr Ile Thr Val Ala Leu Leu Ile Trp Asn Phe Gly	866		
195	200	205	
GTG GTG GGA ATG ATT TCC ATT CAC TGG AAA GGT CCA CTT CGA CTC CAG Val Val Gly Met Ile Ser Ile His Trp Lys Gly Pro Leu Arg Leu Gln	914		
210	215	220	
CAG GCA TAT CTC ATT ATG ATT AGT GCC CTC ATG GCC CTG GTG TTT ATC Gln Ala Tyr Leu Ile Met Ile Ser Ala Leu Met Ala Leu Val Phe Ile	962		
225	230	235	
AAG TAC CTC CCT GAA TGG ACT GCG TGG CTC ATC TTG GCT GTG ATT TCA Lys Tyr Leu Pro Glu Trp Thr Ala Trp Leu Ile Leu Ala Val Ile Ser	1010		
240	245	250	
GTA TAT GAT TTA GTG GCT GTT TTG CGT CTG AAA GGT CCA CTT CAT ATG Val Tyr Asp Leu Val Ala Val Leu Arg Leu Lys Gly Pro Leu His Met	1058		
255	260	265	270
CTG GTT GAA ACA GCT CAG GAG AGA AAT GAA ACG CTT TTT CCA GCT CTC Leu Val Glu Thr Ala Gln Glu Arg Asn Glu Thr Leu Phe Pro Ala Leu	1106		
275	280	285	
ATT TAC TCC TCA ACA ATG GTG TGG TTG GTG AAT ATG GCA GAA GGA GAC Ile Tyr Ser Ser Thr Met Val Trp Leu Val Asn Met Ala Glu Gly Asp	1154		
290	295	300	
CCG GAA GCT CAA AGG AGA GTA TCC AAA AAT TCC AAG CAT AAT GCA GAA Pro Glu Ala Gln Arg Arg Val Ser Lys Asn Ser Lys His Asn Ala Glu	1202		
305	310	315	

AGC ACA GAA AGG GAG TCA CAA GAC ACT GTT GCA GAG AAT GAT GAT GGC Ser Thr Glu Arg Glu Ser Gln Asp Thr Val Ala Glu Asn Asp Asp Gly 320 325 330	1250
GGG TTC AGT GAG GAA TGG GAA GCC CAG AGG GAC AGT CAT CTA GGG CCT Gly Phe Ser Glu Glu Trp Glu Ala Gln Arg Asp Ser His Leu Gly Pro 335 340 345 350	1298
CAT CGC TCT ACA CCT GAG TCA CGA GCT GCT GTC CAG GAA CTT TCC AGC His Arg Ser Thr Pro Glu Ser Arg Ala Ala Val Gln Glu Leu Ser Ser 355 360 365	1346
AGT ATC CTC GCT GGT GAA GAC CCA GAG GAA AGG GGA GTA AAA CTT GGA Ser Ile Leu Ala Gly Glu Asp Pro Glu Glu Arg Gly Val Lys Leu Gly 370 375 380	1394
TTG GGA GAT TTC ATT TTC TAC AGT GTT CTG GTT GGT AAA GCC TCA GCA Leu Gly Asp Phe Ile Phe Tyr Ser Val Leu Val Gly Val Lys Ala Ser Ala 385 390 395	1442
ACA GCC AGT GGA GAC TGG AAC ACA ACC ATA GCC TGT TTC GTA GCC ATA Thr Ala Ser Gly Asp Trp Asn Thr Thr Ile Ala Cys Phe Val Ala Ile 400 405 410	1490
TTA ATT GGT TTG TGC CTT ACA TTA TTA CTC CTT GCC ATT TTC AAG AAA Leu Ile Gly Leu Cys Leu Thr Leu Leu Leu Ala Ile Phe Lys Lys 415 420 425 430	1538
GCA TTG CCA GCT CTT CCA ATC TCC ATC ACC TTT GGS CTT GTT TTC TAC Ala Leu Pro Ala Leu Pro Ile Ser Ile Thr Phe Gly Leu Val Phe Tyr 435 440 445	1586
TTT GCC ACA GAT TAT CTT GTA CAG CCT TTT ATG GAC CAA TTA GCA TTC Phe Ala Thr Asp Tyr Leu Val Gln Pro Phe Met Asp Gln Leu Ala Phe 450 455 460	1634
CAT CAA TTT TAT ATC TAGCATATT GCGGTTAGAA TCCCATGGAT GTTCTCTCTT His Gln Phe Tyr Ile 465	1689
TGACTATAAC CAAATCTGGG GAGGACAAAG GTGATTTTCC TGTGTCCACA TCTAACAAAG	1749
TCAAGATTCC CGGCTGSACT TTTGCAGCTT CCTTCCAAGT CTTCCTGACC ACCTTGCACT	1809
ATTGGACTTT GSAAGGAGGT GCCTATAGAA AACGATTTTG AACATACTTC ATCGCAGTGG	1869
ACTGTGTCCC TCGGTGCAGA AACTACCAGA TTTGAGGGAC GAGGTCAAGG AGATATGATA	1929
GGCCCGGAAG TTGCTGTGCC CCATCAGCAG CTTGACGCGT GGTCACAGGA CGATTTCACT	1989
GACACTGCGA ACTCTCAGGA CTACCGGTTA CCAAGAGGTT AGGTGAAGTG GTTTAAACCA	2049
AACGGAACCT TTCATCTTAA ACTACACGTT GAAAATCAAC CCAATAATTC TGTATTAAC	2109
GAATTCTGAA CTTTTAGGA GGTACTGTGA GGAAGAGCAG GCACCAGCAG CAGAATGGGG	2169
AATGGAGAGG TGGGCAGGGG TTCCAGCTTC CCITTTGATT TTGTCTGCAG ACTCATCCTT	2229
TTTAAATGAG ACTTGTCTTC CCCTCTCTTT GAGTCAAGTC AAATATGTAG ATTGCCITTTG	2289
GCAATTCTTC TTCTCAAGCA CTGACACTCA TTACCGTCTG TGATTGCCAT TCTTCCCAA	2349

GGCCAGTCTG AACCTGAGGT TGCTTTATCC TAAAAGTTTT AACCTCAGGT TCCAAATTCA	2409
GTAAATTTTG GAAACAGTAC AGCTATTCTT CATCAATTCT CTATCATGTT GAAGTCAAAT	2469
TTGGATTTC CACCAAATTC TGAATTTGTA GACATACCTG TAGCGTCACT TGCCCCCAGA	2529
TGCCCTCCTT GTCCTCATTC TTCTCTCCCA CACAAGCAGT CTTTTCTTAC AGCCAGTAAG	2589
GCAGCTCTGT CRTGGTAGCA GATGGTCCCA TTATTCTAGG GTCTTACTCT TTGTATGATG	2649
AAAAGATGT GTTATGAATC GGTGCTGTCA GCCCTGCTGT CAGACCTTCT TCCACAGCAA	2709
ATGAGATGTA TGCCCCAAGC GGTAGAATTA AAGAAGAGTA AAATGGCTGT TGAAGC	2765

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 467 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met	Thr	Glu	Leu	Pro	Ala	Pro	Leu	Ser	Tyr	Phe	Gln	Asn	Ala	Gln	Met
1				5					10					15	
Ser	Glu	Asp	Asn	His	Leu	Ser	Asn	Thr	Val	Arg	Ser	Gln	Asn	Asp	Asn
			20					25					30		
Arg	Glu	Arg	Gln	Glu	His	Asn	Asp	Arg	Arg	Ser	Leu	Gly	His	Pro	Glu
			35				40					45			
Pro	Leu	Ser	Asn	Gly	Arg	Pro	Gln	Gly	Asn	Ser	Arg	Gln	Val	Val	Glu
			50				55				60				
Gln	Asp	Glu	Glu	Glu	Asp	Glu	Glu	Leu	Thr	Leu	Lys	Tyr	Gly	Ala	Lys
	65				70					75					80
His	Val	Ile	Met	Leu	Phe	Val	Pro	Val	Thr	Leu	Cys	Met	Val	Val	Val
			85						90					95	
Val	Ala	Thr	Ile	Lys	Ser	Val	Ser	Phe	Tyr	Thr	Arg	Lys	Asp	Gly	Gln
			100					105					110		
Leu	Ile	Tyr	Thr	Pro	Phe	Thr	Glu	Asp	Thr	Glu	Thr	Val	Gly	Gln	Arg
		115					120					125			
Ala	Leu	His	Ser	Ile	Leu	Asn	Ala	Ala	Ile	Met	Ile	Ser	Val	Ile	Val
			130				135					140			
Val	Met	Thr	Ile	Leu	Leu	Val	Val	Leu	Tyr	Lys	Tyr	Arg	Cys	Tyr	Lys
	145				150					155					160
Val	Ile	His	Ala	Trp	Leu	Ile	Ile	Ser	Ser	Leu	Leu	Leu	Leu	Phe	Phe
			165					170						175	
Phe	Ser	Phe	Ile	Tyr	Leu	Gly	Glu	Val	Phe	Lys	Thr	Tyr	Asn	Val	Ala
			180				185						190		
Val	Asp	Tyr	Ile	Thr	Val	Ala	Leu	Leu	Ile	Trp	Asn	Phe	Gly	Val	Val

195	200	205
Gly Met Ile Ser Ile His Trp Lys Gly Pro Leu Arg Leu Gln Gln Ala 210 215 220		
Tyr Leu Ile Met Ile Ser Ala Leu Met Ala Leu Val Phe Ile Lys Tyr 225 230 235 240		
Leu Pro Glu Trp Thr Ala Trp Leu Ile Leu Ala Val Ile Ser Val Tyr 245 250 255		
Asp Leu Val Ala Val Leu Arg Leu Lys Gly Pro Leu His Met Leu Val 260 265 270		
Glu Thr Ala Gln Glu Arg Asn Glu Thr Leu Phe Pro Ala Leu Ile Tyr 275 280 285		
Ser Ser Thr Met Val Trp Leu Val Asn Met Ala Glu Gly Asp Pro Glu 290 295 300		
Ala Gln Arg Arg Val Ser Lys Asn Ser Lys His Asn Ala Glu Ser Thr 305 310 315 320		
Glu Arg Glu Ser Gln Asp Thr Val Ala Glu Asn Asp Asp Gly Gly Phe 325 330 335		
Ser Glu Glu Trp Glu Ala Gln Arg Asp Ser His Leu Gly Pro His Arg 340 345 350		
Ser Thr Pro Glu Ser Arg Ala Ala Val Gln Glu Leu Ser Ser Ser Ile 355 360 365		
Leu Ala Gly Glu Asp Pro Glu Glu Arg Gly Val Lys Leu Gly Leu Gly 370 375 380		
Asp Phe Ile Phe Tyr Ser Val Leu Val Gly Lys Ala Ser Ala Thr Ala 385 390 395 400		
Ser Gly Asp Trp Asn Thr Thr Ile Ala Cys Phe Val Ala Ile Leu Ile 405 410 415		
Gly Leu Cys Leu Thr Leu Leu Leu Leu Ala Ile Phe Lys Lys Ala Leu 420 425 430		
Pro Ala Leu Pro Ile Ser Ile Thr Phe Gly Leu Val Phe Tyr Phe Ala 435 440 445		
Thr Asp Tyr Leu Val Gln Pro Phe Met Asp Gln Leu Ala Phe His Gln 450 455 460		
Phe Tyr Ile 465		

(2) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

CACCCATTTA CAAGTTTAGC

20

(2) INFORMATION FOR SEQ ID NO: 6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

GATGAGACAA GTGCCGTGAA

20

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Gly Gln Ala Ala Pro Gly Ser Ala Val Ser His Arg Lys Gln Asn Ser
1 5 10 15

Gly Trp Ser Gly Arg Asn Leu Ser Tyr Glu Pro Arg Arg Gln Arg Gly
20 25 30

Gly Gly Glu Ala Tyr Thr
35

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Ser Gly Ser Leu Gln Val Thr Thr Ala Phe Ala Val Leu Arg Gln Leu
1 5 10 15

Gly Leu Glu Glu Asn Thr
20

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Lys Lys Glu Pro Gln Glu Ala Leu Phe Ser Val Lys Gln Tyr Phe Tyr
1 5 10 15

Thr Val Ala Pro
20

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

His Ile Cys Gly
1

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 60 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Asn Pro Met Asp Val Ser Ser Leu Thr Ile Thr Lys Ser Gly Glu Asp
1 5 10 15

Lys Gly Asp Phe Pro Val Ser Thr Ser Asn Lys Val Lys Ile Pro Gly
20 25 30

Trp Thr Phe Ala Ala Ser Phe Gln Val Phe Leu Thr Thr Leu His Tyr
35 40 45

Trp Thr Leu Glu Gly Gly Ala Tyr Arg Lys Arg Phe
50 55 60

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Thr Tyr Phe Ile Ala Val Asp Cys Val Pro Arg Cys Arg Asn Tyr Gln
1 5 10 15

Ile

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Gly Thr Arg Ser Arg Arg Tyr Asp Arg Pro Gly Ser Cys Cys Ala Pro
1 5 10 15

Ser Ala Ala

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Arg Val Val Thr Gly Arg Phe His
1 5

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

His Cys Glu Leu Ser Gly Leu Pro Val Thr Lys Arg Leu Gly Glu Val
1 5 10 15

Val

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Thr Lys Arg Asn Ser Ser Ser
1 5

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Lys Ser Thr Gln
1

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 4 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Phe Cys Ile Asn
1

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

File Leu Asn Phe Ser Gly Gly Thr Val Arg Lys Ser Arg His Gln Gln
1 5 10 15

Gln Asn Gly Glu Trp Arg Gly Gly Gln Gly Phe Gln Leu Pro Phe Asp
20 25 30

Phe Leu Leu Gln Thr His Pro Phe
35 40

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Met Arg Leu Val Phe Pro Ser Leu
1 5

(2) INFORMATION FOR SEQ ID NO:21:

(ii) MOLECULE TYPE: peptide

Val Lys Ser Asn Met
1 5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Ile Ala Phe Gly Asn Ser Ser Ser Gln Ala Leu Thr Leu Ile Thr Val
1 5 10 15

Cys Asp Cys His Phe Phe Pro Arg Pro Val
20 25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Gly Cys Phe Ile Leu Lys Val Leu Thr Ser Gly Ser Lys Phe Ser Lys
1 5 10 15
Phe Trp Phe Lys Gln Tyr Ser Tyr Phe Ser Ser Ile Leu Tyr His Val Glu
20 25 30
Val Lys Phe Gly Phe Ser Thr Lys Phe
35 40

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Ile	Cys	Arg	His	Thr	Cys	Thr	Leu	Thr	Cys	Pro	Gln	Met	Pro	Pro	Leu
1				5				10					15		
Ser	Ser	Phe	Phe	Ser	Pro	Thr	Gln	Ala	Val	Phe	Phe	Tyr	Ser	Gln	
			20				25					30			

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Gly	Ser	Ser	Val	Xaa	Val	Ala	Asp	Gly	Pro	Ile	Ile	Leu	Gly	Ser	Tyr
1				5				10					15		
Ser	Leu	Tyr	Asp	Glu	Lys	Asn	Val	Leu							
			20				25								

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Ile	Gly	Ala	Val	Ser	Pro	Ala	Val	Arg	Pro	Ser	Ser	Thr	Ala	Asn	Glu
1				5				10					15		
Met	Tyr	Ala	Gln	Ser	Gly	Arg	Ile	Lys	Glu	Glu					
			20				25								

(2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2765 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION:249..1649

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

TGGGACAGGC AGCTCCGGGG TCCGCGGTTT CACATCGGAA ACAAAACAGC GGCTGGTCTG	60
GAAGGAACCT GAGCTACGAG CCGCGGCGGC AGCGGGGCGG CGGGGAAGCG TATACCTAAT	120
CTGGGAGCCT GCAAGTGACA ACAGCCTTTG CGGTCCTTAG ACAGCTTGGC CTGGAGGAGA	180
ACACATGAAA GAAAGAACCT CAAGAGGCTT TGTTTTCTGT GAAACAGTAT TTCTATACAG	240
TTGCTCCA ATG ACA GAG TTA CCT GCA CCG TTG TCC TAC TTC CAG AAT GCA	290
Met Thr Glu Leu Pro Ala Pro Leu Ser Tyr Phe Gln Asn Ala	
1 5 10	
CAG ATG TCT GAG GAC AAC CAC CTG AGC AAT ACT GTA CGT AGC CAG AAT	338
Gln Met Ser Glu Asp Asn His Leu Ser Asn Thr Val Arg Ser Gln Asn	
15 20 25 30	
GAC AAT AGA GAA CGG CAG GAG CAC AAC GAC AGA CGG AGC CTT GGC CAC	386
Asp Asn Arg Glu Arg Gln Glu His Asn Asp Arg Arg Ser Leu Gly His	
35 40 45	
CCT GAG CCA TTA TCT AAT GGA CGA CCC CAG GGT AAC TCC CGG CAG GTG	434
Pro Glu Pro Leu Ser Asn Gly Arg Pro Gln Gly Asn Ser Arg Gln Val	
50 55 60	
GTG GAG CAA GAT GAG GAA GAA GAT GAG GAG CTG ACA TTG AAA TAT GGC	482
Val Glu Gln Asp Glu Glu Glu Asp Glu Glu Leu Thr Leu Lys Tyr Gly	
65 70 75	
GCC AAG CAT GTG ATC ATG CTC TTT GTC CCT GTG ACT CTC TGC ATG GTG	530
Ala Lys His Val Ile Met Leu Phe Val Pro Val Thr Leu Cys Met Val	
80 85 90	
GTG GTC GTG GCT ACC ATT AAG TCA GTC AGC TTT TAT ACC CGG AAG GAT	578
Val Val Val Ala Thr Ile Lys Ser Val Ser Phe Tyr Thr Arg Lys Asp	
95 100 105 110	
GGG CAG CTA ATC TAT ACC CCA TTC ACA GAA GAT ACC GAG ACT GTG GGC	626
Gly Gln Leu Ile Tyr Thr Pro Phe Thr Glu Asp Thr Glu Thr Val Gly	
115 120 125	
CAG AGA GCC CTG CAC TCA ATT CTG AAT GCT GCC ATC ATG ATC AGT GTC	674
Gln Arg Ala Leu His Ser Ile Leu Asn Ala Ala Ile Met Ile Ser Val	
130 135 140	
ATT GTT GTC ATG ACT ATC CTC CTG GTG GTT CTG TAT AAA TAC AGG TGC	722

Ile	Val	Val	Met	Thr	Ile	Leu	Leu	Val	Val	Leu	Tyr	Lys	Tyr	Arg	Cys	
		145					150					155				
TAT	AAG	GTC	ATC	CAT	GCC	TGG	CTT	ATT	ATA	TCA	TCT	CTA	TTG	TTG	CTG	770
Tyr	Lys	Val	Ile	His	Ala	Trp	Leu	Ile	Ile	Ser	Ser	Leu	Leu	Leu	Leu	
		160				165					170					
TTC	TTT	TTT	TCA	TTC	ATT	TAC	TTG	GGG	GAA	GTG	TTT	AAA	ACC	TAT	AAC	818
Phe	Phe	Phe	Ser	Phe	Ile	Tyr	Leu	Gly	Glu	Val	Phe	Lys	Thr	Tyr	Asn	
		175			180					185					190	
GTT	GCT	GTG	GAC	TAC	ATT	ACT	GTT	GCA	CTC	CTG	ATC	TGG	AAT	TTT	GGT	866
Val	Ala	Val	Asp	Tyr	Ile	Thr	Val	Ala	Leu	Leu	Ile	Trp	Asn	Phe	Gly	
				195					200					205		
GTG	GTG	GGA	ATG	ATT	TCC	ATT	CAC	TGG	AAA	GGT	CCA	CTT	CGA	CTC	CAG	914
Val	Val	Gly	Met	Ile	Ser	Ile	His	Trp	Lys	Gly	Pro	Leu	Arg	Leu	Gln	
			210					215					220			
CAG	GCA	TAT	CTC	ATT	ATG	ATT	AGT	GCC	CTC	ATG	GCC	CTG	GTG	TTT	ATC	962
Gln	Ala	Tyr	Leu	Ile	Met	Ile	Ser	Ala	Leu	Met	Ala	Leu	Val	Phe	Ile	
			225				230					235				
AAG	TAC	CTC	CCT	GAA	TGG	ACT	GCG	TGG	CTC	ATC	TTG	GCT	GTG	ATT	TCA	1010
Lys	Tyr	Leu	Pro	Glu	Trp	Thr	Ala	Trp	Leu	Ile	Leu	Ala	Val	Ile	Ser	
			240			245					250					
GTA	TAT	GAT	TTA	GTG	GCT	GTT	TTG	CGT	CCG	AAA	GGT	CCA	CTT	CGT	ATG	1058
Val	Tyr	Asp	Leu	Val	Ala	Val	Leu	Arg	Pro	Lys	Gly	Pro	Leu	Arg	Met	
				260					265					270		
CTG	GTT	GAA	ACA	GCT	CAG	GAG	AGA	AAT	GAA	ACG	CTT	TTT	CCA	GCT	CTC	1106
Leu	Val	Glu	Thr	Ala	Gln	Glu	Arg	Asn	Glu	Thr	Leu	Phe	Pro	Ala	Leu	
				275					280					285		
ATT	TAC	TCC	TCA	ACA	ATG	GTG	TGG	TTG	GTG	AAT	ATG	GCA	GAA	GGA	GAC	1154
Ile	Tyr	Ser	Ser	Thr	Met	Val	Trp	Leu	Val	Asn	Met	Ala	Glu	Gly	Asp	
				290				295					300			
CCG	GAA	GCT	CAA	AGG	AGA	GTA	TCC	AAA	AAT	TCC	AAG	CAT	AAT	GCA	GAA	1202
Pro	Glu	Ala	Gln	Arg	Arg	Val	Ser	Lys	Asn	Ser	Lys	His	Asn	Ala	Glu	
			305				310					315				
AGC	ACA	GAA	AGG	GAG	TCA	CAA	GAC	ACT	GTT	GCA	GAG	AAT	GAT	GAT	GGC	1250
Ser	Thr	Glu	Arg	Glu	Ser	Gln	Asp	Thr	Val	Ala	Ala	Asn	Asp	Asp	Gly	
			320			325					330					
GGG	TTC	AGT	GAG	GAA	TGG	GAA	GCC	CAG	AGG	GAC	AGT	CAT	CTA	GGG	CCT	1298
Gly	Phe	Ser	Glu	Glu	Trp	Glu	Ala	Gln	Arg	Asp	Ser	His	Leu	Gly	Pro	
					340					345				350		
CAT	CGC	TCT	ACA	CCT	GAG	TCA	CGA	GCT	GCT	GTC	CAG	GAA	CTT	TCC	AGC	1346
His	Arg	Ser	Thr	Pro	Glu	Ser	Arg	Ala	Ala	Val	Gln	Glu	Leu	Ser	Ser	
				355					360					365		
AGT	ATC	CTC	GCT	GGT	GAA	GAC	CCA	GAG	GAA	AGG	GGA	GTA	AAA	CTT	GGA	1394
Ser	Ile	Leu	Ala	Gly	Glu	Asp	Pro	Glu	Glu	Arg	Gly	Val	Lys	Leu	Gly	
			370					375					380			
TTG	GGA	GAT	TTC	ATT	TTC	TAC	AGT	GTT	CTG	GTT	GGT	AAA	GCC	TCA	GCA	1442
Leu	Gly	Asp	Phe	Ile	Phe	Tyr	Ser	Val	Leu	Val	Gly	Lys	Ala	Ser	Ala	
			385				390					395				

ACA GCC AGT GGA GAC TGG AAC ACA ACC ATA GCC TGT TTC GTA GCC ATA Thr Ala Ser Gly Asp Trp Asn Thr Thr Ile Ala Cys Phe Val Ala Ile 400 405 410	1490
TTA ATT GGT TTG TGC CTT ACA TTA TTA CTC CTT GCC ATT TTC AAG AAA Leu Ile Gly Leu Cys Leu Thr Leu Leu Leu Ala Ile Phe Lys Lys 415 420 425 430	1538
GCA TTG CCA GCT CTT CCA ATC TCC ATC ACC TTT GGG CTT GTT TTC TAC Ala Leu Pro Ala Leu Pro Ile Ser Ile Thr Phe Gly Leu Val Phe Tyr 435 440 445	1586
TTT GCC ACA GAT TAT CTT GTA CAG CCT TTT ATG GAC CAA TTA GCA TTC Phe Ala Thr Asp Tyr Leu Val Gln Pro Phe Met Asp Gln Leu Ala Phe 450 455 460	1634
CAT CAA TTT TAT ATC TAGCATATTT GCGGTAGAA TCCCATGGAT GTTCTTCTTT His Gln Phe Tyr Ile 465	1689
TGACTATAAC CAATCTGGG GAGGACAAAG GTGATTTTCC TGTGTCCACA TCTAACAAAG	1749
TCAAGATTCC CGGCTGGACT TTTGCAGCTT CCTTCCAAGT CTTCCTGACC ACCTTGCACT	1809
ATTGGACITTT GGAAGGAGGT GCCTATAGAA AACGATTTTG AACATACTTC ATCGCAGTGG	1869
ACTGTGTCCC TCGGTGCAGA AACTACCAGA TTTGAGGGAC GAGGTCAAGG AGATATGATA	1929
GGCCCCGAAG TTGCTGTGCC CCATCAGCAG CTTGACGCGT GGTCACAGGA CGATTTTCACT	1989
GACACTGCGA ACTCTCAGGA CTACCGGTTA CCAAGAGGTT AGGTGAAGTG GTTTAAACCA	2049
AACGGAACTC TTCATCTTAA ACTACACGTT GAAATCAAC CCAATAATTC TGTATTAACT	2109
GAATTCTGAA CTTTTCAGGA GGTACTGTGA GGAAGAGCAG GCACACGACG CAGAATGGGG	2169
AATGGAGAGG TGGGCAGGGG TTCCAGCTTC CCTTTGATTT TTTGCTGCAG ACTCATCCTT	2229
TTTAAATGAG ACTTGTTTTC CCTCTCTTT GAGTCAAGTC AAATATGTAG ATTGCCTTTG	2289
GCAATTTCTC TTCTCAAGCA CTGACACTCA TTACCGTCTG TGATTGCCAT TTCTTCCCAA	2349
GGCCAGTCTG AACCTGAGGT TGCTTTATCC TAAAGTTTT AACCTCAGGT TCCAAATTCA	2409
GTAATTTTTG GAAACAGTAC AGCTATTCTT CATCAATTCT CTATCATGTT GAAGTCAAAAT	2469
TTGGATTTTC CACCAAAATC TGAATTTGTA GACATACTTG TACGCTCACT TGCCCCCAGA	2529
TGCCTCCTCT GTCTCTATTCT TTCTCTCCCA CACAAGCAGT CTTTITCTAC AGCCAGTAAG	2589
GCAGCTCTGT CRTGGTAGCA GATGGTCCCA TTATICTAGG GTCTTACTCT TTGTATGATG	2649
AAAAGAATGT GTTATGAATC GGTGCTGTCA GCCCTGTCTG CAGACCTTCT TCCACAGCAA	2709
ATGAGATGTA TGCCCAAAGC GGTAGAATTA AAGAAGAGTA AAATGGCTGT TGAAGC	2765

(2) INFORMATION FOR SEQ ID NO: 28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 467 amino acids
 - (B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

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Met Thr Glu Leu Pro Ala Pro Leu Ser Tyr Phe Gln Asn Ala Gln Met
 1      5      10      15

Ser Glu Asp Asn His Leu Ser Asn Thr Val Arg Ser Gln Asn Asp Asn
      20      25      30

Arg Glu Arg Gln Glu His Asn Asp Arg Arg Ser Leu Gly His Pro Glu
      35      40      45

Pro Leu Ser Asn Gly Arg Pro Gln Gly Asn Ser Arg Gln Val Val Glu
      50      55      60

Gln Asp Glu Glu Glu Asp Glu Glu Leu Thr Leu Lys Tyr Gly Ala Lys
      65      70      75      80

His Val Ile Met Leu Phe Val Pro Val Thr Leu Cys Met Val Val Val
      85      90      95

Val Ala Thr Ile Lys Ser Val Ser Phe Tyr Thr Arg Lys Asp Gly Gln
      100      105      110

Leu Ile Tyr Thr Pro Phe Thr Glu Asp Thr Glu Thr Val Gly Gln Arg
      115      120      125

Ala Leu His Ser Ile Leu Asn Ala Ala Ile Met Ile Ser Val Ile Val
      130      135      140

Val Met Thr Ile Leu Leu Val Val Leu Tyr Lys Tyr Arg Cys Tyr Lys
      145      150      155      160

Val Ile His Ala Trp Leu Ile Ile Ser Ser Leu Leu Leu Leu Phe Phe
      165      170      175

Phe Ser Phe Ile Tyr Leu Gly Glu Val Phe Lys Thr Tyr Asn Val Ala
      180      185      190

Val Asp Tyr Ile Thr Val Ala Leu Leu Ile Trp Asn Phe Gly Val Val
      195      200      205

Gly Met Ile Ser Ile His Trp Lys Gly Pro Leu Arg Leu Gln Gln Ala
      210      215      220

Tyr Leu Ile Met Ile Ser Ala Leu Met Ala Leu Val Phe Ile Lys Tyr
      225      230      235      240

Leu Pro Glu Trp Thr Ala Trp Leu Ile Leu Ala Val Ile Ser Val Tyr
      245      250      255

Asp Leu Val Ala Val Leu Arg Pro Lys Gly Pro Leu Arg Met Leu Val
      260      265      270

Glu Thr Ala Gln Glu Arg Asn Glu Thr Leu Phe Pro Ala Leu Ile Tyr
      275      280      285

Ser Ser Thr Met Val Trp Leu Val Asn Met Ala Glu Gly Asp Pro Glu
      290      295      300

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Ala Gln Arg Arg Val Ser Lys Asn Ser Lys His Asn Ala Glu Ser Thr
305 310 315 320

Glu Arg Glu Ser Gln Asp Thr Val Ala Glu Asn Asp Asp Gly Gly Phe
325 330 335

Ser Glu Glu Trp Glu Ala Gln Arg Asp Ser His Leu Gly Pro His Arg
340 345 350

Ser Thr Pro Glu Ser Arg Ala Ala Val Gln Glu Leu Ser Ser Ser Ile
355 360 365

Leu Ala Gly Glu Asp Pro Glu Glu Arg Gly Val Lys Leu Gly Leu Gly
370 375 380

Asp Phe Ile Phe Tyr Ser Val Leu Val Gly Lys Ala Ser Ala Thr Ala
385 390 395 400

Ser Gly Asp Trp Asn Thr Thr Ile Ala Cys Phe Val Ala Ile Leu Ile
405 410 415

Gly Leu Cys Leu Thr Leu Leu Leu Ala Ile Phe Lys Lys Ala Leu
420 425 430

Pro Ala Leu Pro Ile Ser Ile Thr Phe Gly Leu Val Phe Tyr Phe Ala
435 440 445

Thr Asp Tyr Leu Val Gln Pro Phe Met Asp Gln Leu Ala Phe His Gln
450 455 460

Phe Tyr Ile
465

(2) INFORMATION FOR SEQ ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2765 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION:249..1649

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

TGGGACAGCG AGCTCCGGGG TCCGCGGTTT CACATCGGAA ACAAAACAGC GGCTGGTCTG	60
GAAGGAACCT GAGCTACGAG CCGCGGCGGC AGCGGGCGCG CGGGGAAGCG TATACCTAAT	120
CTGGGAGCCT GCAAGTGACA ACAGCCTTTG CGGTCCTTAG ACAGCTTGGC CTGGAGGAGA	180
ACACATGAAA GAAAGAACCT CAAGAGGCTT TGTTCCTGT GAAACAGTAT TTCTATACAG	240
TTGCTCCA ATG ACA GAG TTA CCT GCA CCG TTG TCC TAC TTC CAG AAT GCA	290
Met Thr Glu Leu Pro Ala Pro Leu Ser Tyr Phe Gln Asn Ala	

1	5	10	
CAG ATG TCT GAG GAC AAC CAC CTG AGC AAT ACT GTA CGT AGC CAG AAT Gln Met Ser Glu Asp Asn His Leu Ser Asn Thr Val Arg Ser Gln Asn 15 20 25 30			338
GAC AAT AGA GAA CGG CAG GAG CAC AAC GAC AGA CGG AGC CTT GGC CAC Asp Asn Arg Glu Arg Gln Glu His Asn Asp Arg Arg Ser Leu Gly His 35 40 45			386
CCT GAG CCA TTA TCT AAT GGA CGA CCC CAG GGT AAC TCC CGG CAG GTG Pro Glu Pro Leu Ser Asn Gly Arg Pro Gln Gly Asn Ser Arg Gln Val 50 55 60			434
GTG GAG CAA GAT GAG GAA GAA GAT GAG GAG CTG ACA TTG AAA TAT GGC Val Glu Gln Asp Glu Glu Glu Asp Glu Glu Leu Thr Leu Lys Tyr Gly 65 70 75			482
GCC AAG CAT GTG ATC ATG CTC TTT GTC CCT GTG ACT CTC TGC ATG GTG Ala Lys His Val Ile Met Leu Phe Val Pro Val Thr Leu Cys Met Val 80 85 90			530
GTG GTC GTG GCT ACC ATT AAG TCA GTC AGC TTT TAT ACC CGG AAG GAT Val Val Val Ala Thr Ile Lys Ser Val Ser Phe Tyr Thr Arg Lys Asp 95 100 105 110			578
GGG CAG CTA ATC TAT ACC CCA TTC ACA GAA GAT ACC GAG ACT GTG GGC Gly Gln Leu Ile Tyr Thr Pro Phe Thr Glu Asp Thr Glu Thr Val Gly 115 120 125			626
CAG AGA GCC CTG CAC TCA ATT CTG AAT GCT GCC ATC ATG ATC AGT GTC Gln Arg Ala Leu His Ser Ile Leu Asn Ala Ala Ile Met Ile Ser Val 130 135 140			674
ATT GTT GTC ATG ACT ATC CTC CTG GTG GTT CTG TAT AAA TAC AGG TGC Ile Val Val Met Thr Ile Leu Leu Val Val Leu Tyr Lys Tyr Arg Cys 145 150 155			722
TAT AAG GTC ATC CAT GCC TGG CTT ATT ATA TCA TCT CTA TTG TTG CTG Tyr Lys Val Ile His Ala Trp Leu Ile Ile Ser Ser Leu Leu Leu Leu 160 165 170			770
TTC TTT TTT TCA TTC ATT TAC TTG GGG GAA GTG TTT AAA ACC TAT AAC Phe Phe Phe Ser Phe Ile Tyr Leu Gly Glu Val Phe Lys Thr Tyr Asn 175 180 185 190			818
GTT GCT GTG GAC TAC ATT ACT GTT GCA CTC CTG ATC TGG AAT TTT GGT Val Ala Val Asp Tyr Ile Thr Val Ala Leu Leu Ile Trp Asn Phe Gly 195 200 205			866
GTG GTG GGA ATG ATT TCC ATT CAC TGG AAA GGT CCA CTT CGA CTC CAG Val Val Gly Met Ile Ser Ile His Trp Lys Gly Pro Leu Arg Leu Gln 210 215 220			914
CAG GCA TAT CTC ATT ATG ATT AGT GCC CTC ATG GCC CTG GTG TTT ATC Gln Ala Tyr Leu Ile Met Ile Ser Ala Leu Met Ala Leu Val Phe Ile 225 230 235			962
AAG TAC CTC CCT GAA TGG ACT GCG TGG CTC ATC TTG GCT GTG ATT TCA Lys Tyr Leu Pro Glu Trp Thr Ala Trp Leu Ile Leu Ala Val Ile Ser 240 245 250			1010

GTA TAT GAT TTA GTG GCT GTT TTG TGT CTG AAA GGT CCA CTT CGT ATG Val Tyr Asp Leu Val Ala Val Leu Cys Leu Lys Gly Pro Leu Arg Met 255 260 265 270	1058
CTG GTT GAA ACA GCT CAG GAG AGA AAT GAA ACG CTT TTT CCA GCT CTC Leu Val Glu Thr Ala Gln Glu Arg Asn Glu Thr Leu Phe Pro Ala Leu 275 280 285	1106
ATT TAC TCC TCA ACA ATG GTG TGG TTG GTG AAT ATG GCA GAA GGA GAC Ile Tyr Ser Ser Thr Met Val Trp Leu Val Asn Met Ala Glu Gly Asp 290 295 300	1154
CCG GAA GCT CAA AGG AGA GTA TCC AAA AAT TCC AAG CAT AAT GCA GAA Pro Glu Ala Gln Arg Arg Val Ser Lys Asn Ser Lys His Asn Ala Glu 305 310 315	1202
AGC ACA GAA AGG GAG TCA CAA GAC ACT GTT GCA GAG AAT GAT GAT GGC Ser Thr Glu Arg Glu Ser Gln Asp Thr Val Ala Glu Asn Asp Asp Gly 320 325 330	1250
GGG TTC AGT GAG GAA TGG GAA GCC CAG AGG GAC AGT CAT CTA GGG CCT Gly Phe Ser Glu Glu Trp Glu Ala Gln Arg Asp Ser His Leu Gly Pro 335 340 345 350	1298
CAT CGC TCT ACA CCT GAG TCA CGA GCT GCT GTC CAG GAA CTT TCC AGC His Arg Ser Thr Pro Glu Ser Arg Ala Ala Val Gln Glu Leu Ser Ser 355 360 365	1346
AGT ATC CTC GCT GGT GAA GAC CCA GAG GAA AGG GGA GTA AAA CTT GGA Ser Ile Leu Ala Gly Glu Asp Pro Glu Glu Arg Gly Val Lys Leu Gly 370 375 380	1394
TTG GGA GAT TTC ATT TTC TAC AGT GTT CTG GTT GGT AAA GCC TCA GCA Leu Gly Asp Phe Ile Phe Tyr Ser Val Leu Val Gly Lys Ala Ser Ala 385 390 395	1442
ACA GCC AGT GGA GAC TGG AAC ACA ACC ATA GCC TGT TTC GTA GCC ATA Thr Ala Ser Gly Asp Trp Asn Thr Thr Ile Ala Cys Phe Val Ala Ile 400 405 410	1490
TTA ATT GGT TTG TGC CTT ACA TTA TTA CTC CTT GCC ATT TTC AAG AAA Leu Ile Gly Leu Cys Leu Thr Leu Leu Leu Leu Ala Ile Phe Lys Lys 415 420 425 430	1538
GCA TTG CCA GCT CTT CCA ATC TCC ATC ACC TTT GGG CTT GTT TTC TAC Ala Leu Pro Ala Leu Pro Ile Ser Ile Thr Phe Gly Leu Val Phe Tyr 435 440 445	1586
TTT GCC ACA GAT TAT CTT GTA CAG CCT TTT ATG GAC CAA TTA GCA TTC Phe Ala Thr Asp Tyr Leu Val Gln Pro Phe Met Asp Gln Leu Ala Phe 450 455 460	1634
CAT CAA TTT TAT ATC TAGCATATTT GCGGTTAGAA TCCCATGGAT GTTCTCTCTT His Gln Phe Tyr Ile 465	1689
TGACTATAAC CAAATCTGGG GAGGACAAAG GTGATTTTCC TGTGTCCACA TCTAACAAAG	1749
TCAAGATTCC CGGCTGGACT TTTCAGGCTT CCTTCCAAGT CTTCTGACC ACCTTGCACT	1809
ATTGGACTTT GGAAGGAGGT GCCTATAGAA AACGATTITG AACATACTTC ATCGCAGTGG	1869

ACTGTGTCCC TCGGTGCAGA AACTACCAGA TTTGAGGGAC GAGGTCAAGG AGATATGATA 1929
 GGCCCGGAAG TTGCTGTGCC CCATCAGCAG CTTGACGCGT GGTACACAGGA CGATTTCCTACT 1989
 GACACTGCGA ACTCTCAGGA CTACCGGTTA CCAAGAGGTT AGGTGAAGTG GTTTAAACCA 2049
 AACGGAACCT TTCATCTTAA ACTACACGTT GAAAATCAAC CCAATAATTC TGTATTAACCT 2109
 GAATTCTGAA CTTTTCAGGA GGTACTGTGA GGAAGAGCAG GCACCAGCAG CAGAATGGGG 2169
 AATGAGAGAG TGGGCAGGGG TTCCAGCTTC CCTTTGATT TTTGCTGCAG ACTCATCCTT 2229
 TTAAATGAG ACTTGTITTC CCCCTCTCTT GAGTCAAGTC AAATATGTAG ATTGCCCTTG 2289
 GCAATTCTTC TTCTCAAGCA CTGACACTCA TTACCGTCTG TGATTGCCAT TTCTTCCCAA 2349
 GGCCAGTCTG AACCTGAGGT TGCTTTATCC TAAAAGTTTT AACCTCAGGT TCCAAATTC 2409
 GTAAATTTTG GAAACAGTAC AGCTATTCT CATCAATTCT CTATCATGTT GAAGTCAAAT 2469
 TTGGATTTTC CACCAAAATC TGAATTGTGA GACATACTTG TACGCTCACT TGCCCCCAGA 2529
 TGCCTCTCTG GTCCTCATT CTCTCTCCCA CACAAGCAGT CTTTTTCTAC AGCCAGTAAG 2589
 GCAGCTCTGT CRTGGTAGCA GATGGTCCCA TTATTCTAGG GTCTTACTCT TTGTATGATG 2649
 AAAAGAATGT GTTATGAATC GGTGCTGTCA GCCCTGCTGT CAGACCTTCT TCCACAGCAA 2709
 ATGAGATGTA TGCCCAAAGC GGTAGAATTA AAGAAGAGTA AAATGGCTGT TGAAGC 2765

(2) INFORMATION FOR SEQ ID NO: 30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 467 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

Met	Thr	Glu	Leu	Pro	Ala	Pro	Leu	Ser	Tyr	Phe	Gln	Asn	Ala	Gln	Met
1				5					10					15	
Ser	Glu	Asp	Asn	His	Leu	Ser	Asn	Thr	Val	Arg	Ser	Gln	Asn	Asp	Asn
			20					25					30		
Arg	Glu	Arg	Gln	Glu	His	Asn	Asp	Arg	Arg	Ser	Leu	Gly	His	Pro	Glu
			35				40					45			
Pro	Leu	Ser	Asn	Gly	Arg	Pro	Gln	Gly	Asn	Ser	Arg	Gln	Val	Val	Glu
			50			55				60					
Gln	Asp	Glu	Glu	Glu	Asp	Glu	Glu	Leu	Thr	Leu	Lys	Tyr	Gly	Ala	Lys
			65			70				75				80	
His	Val	Ile	Met	Leu	Phe	Val	Pro	Val	Thr	Leu	Cys	Met	Val	Val	Val
			85					90					95		
Val	Ala	Thr	Ile	Lys	Ser	Val	Ser	Phe	Tyr	Thr	Arg	Lys	Asp	Gly	Gln
			100					105					110		

Leu Ile Tyr Thr Pro Phe Thr Glu Asp Thr Glu Thr Val Gly Gln Arg
 115 120 125
 Ala Leu His Ser Ile Leu Asn Ala Ala Ile Met Ile Ser Val Ile Val
 130 135 140
 Val Met Thr Ile Leu Leu Val Val Leu Tyr Lys Tyr Arg Cys Tyr Lys
 145 150 155 160
 Val Ile His Ala Trp Leu Ile Ile Ser Ser Leu Leu Leu Leu Phe Phe
 165 170 175
 Phe Ser Phe Ile Tyr Leu Gly Glu Val Phe Lys Thr Tyr Asn Val Ala
 180 185 190
 Val Asp Tyr Ile Thr Val Ala Leu Leu Ile Trp Asn Phe Gly Val Val
 195 200 205
 Gly Met Ile Ser Ile His Trp Lys Gly Pro Leu Arg Leu Gln Gln Ala
 210 215 220
 Tyr Leu Ile Met Ile Ser Ala Leu Met Ala Leu Val Phe Ile Lys Tyr
 225 230 235 240
 Leu Pro Glu Trp Thr Ala Trp Leu Ile Leu Ala Val Ile Ser Val Tyr
 245 250 255
 Asp Leu Val Ala Val Leu Cys Leu Lys Gly Pro Leu Arg Met Leu Val
 260 265 270
 Glu Thr Ala Gln Glu Arg Asn Glu Thr Leu Phe Pro Ala Leu Ile Tyr
 275 280 285
 Ser Ser Thr Met Val Trp Leu Val Asn Met Ala Glu Gly Asp Pro Glu
 290 295 300
 Ala Gln Arg Arg Val Ser Lys Asn Ser Lys His Asn Ala Glu Ser Thr
 305 310 315 320
 Glu Arg Glu Ser Gln Asp Thr Val Ala Glu Asn Asp Asp Gly Gly Phe
 325 330 335
 Ser Glu Glu Trp Glu Ala Gln Arg Asp Ser His Leu Gly Pro His Arg
 340 345 350
 Ser Thr Pro Glu Ser Arg Ala Ala Val Gln Glu Leu Ser Ser Ser Ile
 355 360 365
 Leu Ala Gly Glu Asp Pro Glu Glu Arg Gly Val Lys Leu Gly Leu Gly
 370 375 380
 Asp Phe Ile Phe Tyr Ser Val Leu Val Gly Lys Ala Ser Ala Thr Ala
 385 390 395 400
 Ser Gly Asp Trp Asn Thr Thr Ile Ala Cys Phe Val Ala Ile Leu Ile
 405 410 415
 Gly Leu Cys Leu Thr Leu Leu Leu Leu Ala Ile Phe Lys Lys Ala Leu
 420 425 430
 Pro Ala Leu Pro Ile Ser Ile Thr Phe Gly Leu Val Phe Tyr Phe Ala
 435 440 445

Thr Asp Tyr Leu Val Gln Pro Phe Met Asp Gln Leu Ala Phe His Gln
450 455 460

Phe Tyr Ile
465

(2) INFORMATION FOR SEQ ID NO: 31:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2765 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION:249..1649

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

TGGGACAGGC AGCTCCGGGG TCCGCGGTTT CACATCGGAA ACAAACAGC GGCTGGTCTG	60
GAAGGAACCT GAGCTACGAG CCGCGGCGGC AGCGGGGCGG CGGGGAAGCG TATACCTAAT	120
CTGGGAGCCT GCAAGTGACA ACAGCCTTTG CGGTCTTAG ACAGCTTGGC CTGGAGGAGA	180
ACACATGAAA GAAAGAACCT CAAGAGGCTT TGTTTCTGT GAAACAGTAT TTCATACAG	240
TTGCTCCA ATG ACA GAG TTA CCT GCA CCG TTG TCC TAC TTC CAG AAT GCA	290
Met Thr Glu Leu Pro Ala Pro Leu Ser Tyr Phe Gln Asn Ala	
1 5 10	
CAG ATG TCT GAG GAC AAC CAC CTG AGC AAT ACT GTA CGT AGC CAG AAT	338
Gln Met Ser Glu Asp Asn His Leu Ser Asn Thr Val Arg Ser Gln Asn	
15 20 25 30	
GAC AAT AGA GAA CGG CAG GAG CAC AAC GAC AGA CGG AGC CTT GGC CAC	386
Asp Asn Arg Glu Arg Gln Glu His Asn Asp Arg Arg Ser Leu Gly His	
35 40 45	
CCT GAG CCA TTA TCT AAT GGA CGA CCC CAG GGT AAC TCC CGG CAG GTG	434
Pro Glu Pro Leu Ser Asn Gly Arg Pro Gln Gly Asn Ser Arg Gln Val	
50 55 60	
GTG GAG CAA GAT GAG GAA GAA GAT GAG GAG CTG ACA TTG AAA TAT GGC	482
Val Glu Gln Asp Glu Glu Glu Asp Glu Glu Leu Thr Leu Lys Tyr Gly	
65 70 75	
GCC AAG CAT GTG ATC ATG CTC TTT GTC CCT GTG ACT CTC TGC ATG GTG	530
Ala Lys His Val Ile Met Leu Phe Val Pro Val Thr Leu Cys Met Val	
80 85 90	
GTG GTC GTG GCT ACC ATT AAG TCA GTC AGC TTT TAT ACC CGG AAG GAT	578
Val Val Val Ala Thr Ile Lys Ser Val Ser Phe Tyr Thr Arg Lys Asp	
95 100 105 110	
GGG CAG CTA ATC TAT ACC CCA TTC ACA GAA GAT ACC GAG ACT GTG GGC	626

Gly	Gln	Leu	Ile	Tyr	Thr	Pro	Phe	Thr	Glu	Asp	Thr	Glu	Thr	Val	Gly	
				115					120					125		
CAG	AGA	GCC	CTG	CAC	TCA	ATT	CTG	AAT	GCT	GCC	ATC	ATG	ATC	AGT	GTC	674
Gln	Arg	Ala	Leu	His	Ser	Ile	Leu	Asn	Ala	Ala	Ile	Met	Ile	Ser	Val	
			130					135					140			
ATT	GTT	GTC	ATG	ACT	ATC	CTC	CTG	GTG	GTT	CTG	TAT	AAA	TAC	AGG	TGC	722
Ile	Val	Val	Met	Thr	Ile	Leu	Leu	Val	Val	Leu	Tyr	Lys	Tyr	Arg	Cys	
			145				150					155				
TAT	AAG	GTC	ATC	CAT	GCC	TGG	CTT	ATT	ATA	TCA	TCT	CTA	TTG	TTG	CTG	770
Tyr	Lys	Val	Ile	His	Ala	Trp	Leu	Ile	Ile	Ser	Ser	Leu	Leu	Leu	Leu	
	160					165					170					
TTC	TTT	TTT	TCA	TTC	ATT	TAC	TTG	GGG	GAA	GTG	TTT	AAA	ACC	TAT	AAC	818
Phe	Phe	Phe	Ser	Phe	Ile	Tyr	Leu	Gly	Glu	Val	Phe	Lys	Thr	Tyr	Asn	
					180					185					190	
GTT	GCT	GTG	GAC	TAC	ATT	ACT	GTT	GCA	CTC	CTG	ATC	TGG	AAT	TTT	GGT	866
Val	Ala	Val	Asp	Tyr	Ile	Thr	Val	Ala	Leu	Leu	Ile	Trp	Asn	Phe	Gly	
				195					200					205		
GTG	GTG	GGA	ATG	ATT	TCC	ATT	CAC	TGG	AAA	GGT	CCA	CTT	CGA	CTC	CAG	914
Val	Val	Gly	Met	Ile	Ser	Ile	His	Trp	Lys	Gly	Pro	Leu	Arg	Leu	Gln	
			210					215					220			
CAG	GCA	TAT	CTC	ATT	ATG	ATT	AGT	GCC	CTC	ATG	GCC	CTG	GTG	TTT	ATC	962
Gln	Ala	Tyr	Leu	Ile	Met	Ile	Ser	Ala	Leu	Met	Ala	Leu	Val	Phe	Ile	
			225				230					235				
AAG	TAC	CTC	CCT	GAA	TGG	ACT	GCG	TGG	CTC	ATC	TTG	GCT	GTG	ATT	TCA	1010
Lys	Tyr	Leu	Pro	Glu	Trp	Thr	Ala	Trp	Leu	Ile	Leu	Ala	Val	Ile	Ser	
	240					245					250					
GTA	TAT	GAT	TTA	GTG	GCT	GTT	TTG	TGT	CCG	AAA	GGT	CCA	CTT	CAT	ATG	1058
Val	Tyr	Asp	Leu	Val	Ala	Val	Leu	Cys	Pro	Lys	Gly	His	Pro	Leu	His	
					260					265					270	
CTG	GTT	GAA	ACA	GCT	CAG	GAG	AGA	AAT	GAA	ACG	CTT	TTT	CCA	GCT	CTC	1106
Leu	Val	Glu	Thr	Ala	Gln	Glu	Arg	Asn	Glu	Thr	Leu	Phe	Pro	Ala	Leu	
				275					280					285		
ATT	TAC	TCC	TCA	ACA	ATG	GTG	TGG	TTG	GTG	AAT	ATG	GCA	GAA	GGA	GAC	1154
Ile	Tyr	Ser	Ser	Thr	Met	Val	Trp	Leu	Val	Asn	Met	Ala	Glu	Gly	Asp	
				290				295					300			
CCG	GAA	GCT	CAA	AGG	AGA	GTA	TCC	AAA	AAT	TCC	AAG	CAT	AAT	GCA	GAA	1202
Pro	Glu	Ala	Gln	Arg	Arg	Val	Ser	Lys	Asn	Ser	Lys	His	Asn	Ala	Glu	
			305				310					315				
AGC	ACA	GAA	AGG	GAG	TCA	CAA	GAC	ACT	GTT	GCA	GAG	AAT	GAT	GAT	GGC	1250
Ser	Thr	Glu	Arg	Glu	Ser	Gln	Asp	Thr	Val	Ala	Glu	Asn	Asp	Asp	Gly	
			320			325					330					
GGG	TTC	AGT	GAG	GAA	TGG	GAA	GCC	CAG	AGG	GAC	AGT	CAT	CTA	GGG	CCT	1298
Gly	Phe	Ser	Glu	Glu	Trp	Glu	Ala	Gln	Arg	Asp	Ser	His	Leu	Gly	Pro	
					340					345					350	
CAT	CGC	TCT	ACA	CCT	GAG	TCA	CGA	GCT	GCT	GTC	CAG	GAA	CTT	TCC	AGC	1346
His	Arg	Ser	Thr	Pro	Glu	Ser	Arg	Ala	Ala	Val	Gln	Glu	Leu	Ser	Ser	
				355				360						365		

AGT ATC CTC GCT GGT GAA GAC CCA GAG GAA AGG GGA GTA AAA CTT GGA Ser Ile Leu Ala Gly Glu Asp Pro Glu Glu Arg Gly Val Lys Leu Gly 370 375 380	1394
TTG GGA GAT TTC ATT TTC TAC AGT GTT CTG GTT GGT AAA GCC TCA GCA Leu Gly Asp Phe Ile Phe Tyr Ser Val Leu Val Gly Lys Ala Ser Ala 385 390 395	1442
ACA GCC AGT GGA GAC TGG AAC ACA ACC ATA GCC TGT TTC GTA GCC ATA Thr Ala Ser Gly Asp Trp Asn Thr Thr Ile Ala Cys Phe Val Ala Ile 400 405 410	1490
TTA ATT GGT TTG TGC CTT ACA TTA TTA CTC CTT GCC ATT TTC AAG AAA Leu Ile Gly Leu Cys Leu Thr Leu Leu Leu Ala Ile Phe Lys Lys 415 420 425 430	1538
GCA TTG CCA GCT CTT CCA ATC TCC ATC ACC TTT GGG CTT GTT TTC TAC Ala Leu Pro Ala Leu Pro Ile Ser Ile Thr Phe Gly Leu Val Phe Tyr 435 440 445	1586
TTT GCC ACA GAT TAT CTT GTA CAG CCT TTT ATG GAC CAA TTA GCA TTC Phe Ala Thr Asp Tyr Leu Val Gln Pro Phe Met Asp Gln Leu Ala Phe 450 455 460	1634
CAT CAA TTT TAT ATC TAGCATATTT GCGGTTAGAA TCCCATGGAT GTTCTCTCTT His Gln Phe Tyr Ile 465	1689
TGACTATAAC CAAATCTGGG GAGGACAAAG GTGATTITTC TGTGTCCACA TCTAACAAAG	1749
TCAAGATTCC CGGCTGGACT TTTGCAGCTT CCTTCCAAGT CTTCCTGACC ACCTTGCACT	1809
ATTGGACTTT GGAAGGAGGT GCCTATAGAA AACGATTTTG AACATACTTC ATCGCAGTGG	1869
ACTGTGTCCC TCGGTGCAGA AACTACCAGA TTTGAGGGAC GAGGTCAAGG AGATATGATA	1929
GGCCCGGAAG TTGCTGTGCC CCATCAGCAG CTTGACGCGT GGTCACAGGA CGATTTCACCT	1989
GACACTGCGA ACTCTCAGGA CTACCGGTTA CCAAGAGGTT AGSTGAAGTG GTTTAAACCA	2049
AACGGAACCT TTCATCTTAA ACTACACGTT GAAAATCAAC CCAATAATTC TGTATTAACT	2109
GAATTCTGAA CTTTTCAGGA GGTACTGTGA GGAAGAGCAG GCACCAGCAG CAGAATGGGG	2169
AATGGAGAGG TGGGCAGGGG TTCCAGCTTC CCTTTGATTT TTTGCTGCAG ACTCATCCTT	2229
TTTAAATGAG ACTTGTTTTC CCCCTCTCTT GAGTCAAGTC AAATATGTAG ATTGCCCTTG	2289
GCAATTCTTC TTCTCAAGCA CTGACACTCA TTACCGTCTG TGATTGCCAT TTCTTCCCAA	2349
GGCCAGTCTG AACCTGAGGT TGCTTTATCC TAAAAGTTTT AACCTCAGGT TCCAAATTCA	2409
GTAAATTTTG GAAACAGTAC AGCTATTTCT CATCAATTCT CTATCATGTT GAAGTCAAAAT	2469
TTGGATTTTC CACCAAAATC TGAATTTGTA GACATACTTG TACGCTCACT TGCCCCCAGA	2529
TGCCCTCTCT GTCCCTCATTC TTCTCTCCCA CACAAGCAGT CTTTTCTTAC AGCCAGTAAG	2589
GCAGCTCTGT CRTGGTAGCA GATGGTCCCA TTATTCTAGG GTCTTACTCT TTGTATGATG	2649
AAAAGAATGT GTTATGAATC GGTGCTGTCA GCCCTGCTGT CAGACCTTCT TCCACAGCAA	2709

ATGAGATGTA TGCCCAAAGC GGTAGAATTA AAGAAGAGTA AAATGGCTGT TGAAGC

2765

(2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 467 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

Met	Thr	Glu	Leu	Pro	Ala	Pro	Leu	Ser	Tyr	Phe	Gln	Asn	Ala	Gln	Met
1				5					10					15	
Ser	Glu	Asp	Asn	His	Leu	Ser	Asn	Thr	Val	Arg	Ser	Gln	Asn	Asp	Asn
			20					25					30		
Arg	Glu	Arg	Gln	Glu	His	Asn	Asp	Arg	Arg	Ser	Leu	Gly	His	Pro	Glu
			35					40				45			
Pro	Leu	Ser	Asn	Gly	Arg	Pro	Gln	Gly	Asn	Ser	Arg	Gln	Val	Val	Glu
			50				55				60				
Gln	Asp	Glu	Glu	Glu	Asp	Glu	Glu	Leu	Thr	Leu	Lys	Tyr	Gly	Ala	Lys
	65				70					75					80
His	Val	Ile	Met	Leu	Phe	Val	Pro	Val	Thr	Leu	Cys	Met	Val	Val	Val
			85						90					95	
Val	Ala	Thr	Ile	Lys	Ser	Val	Ser	Phe	Tyr	Thr	Arg	Lys	Asp	Gly	Gln
			100					105						110	
Leu	Ile	Tyr	Thr	Pro	Phe	Thr	Glu	Asp	Thr	Glu	Thr	Val	Gly	Gln	Arg
			115				120						125		
Ala	Leu	His	Ser	Ile	Leu	Asn	Ala	Ala	Ile	Met	Ile	Ser	Val	Ile	Val
			130				135					140			
Val	Met	Thr	Ile	Leu	Leu	Val	Val	Leu	Tyr	Lys	Tyr	Arg	Cys	Tyr	Lys
	145				150					155					160
Val	Ile	His	Ala	Trp	Leu	Ile	Ile	Ser	Ser	Leu	Leu	Leu	Leu	Phe	Phe
				165					170					175	
Phe	Ser	Phe	Ile	Tyr	Leu	Gly	Glu	Val	Phe	Lys	Thr	Tyr	Asn	Val	Ala
			180					185						190	
Val	Asp	Tyr	Ile	Thr	Val	Ala	Leu	Leu	Ile	Trp	Asn	Phe	Gly	Val	Val
			195				200					205			
Gly	Met	Ile	Ser	Ile	His	Trp	Lys	Gly	Pro	Leu	Arg	Leu	Gln	Gln	Ala
			210				215					220			
Tyr	Leu	Ile	Met	Ile	Ser	Ala	Leu	Met	Ala	Leu	Val	Phe	Ile	Lys	Tyr
	225					230				235					240
Leu	Pro	Glu	Trp	Thr	Ala	Trp	Leu	Ile	Leu	Ala	Val	Ile	Ser	Val	Tyr
				245					250					255	
Asp	Leu	Val	Ala	Val	Leu	Cys	Pro	Lys	Gly	Pro	Leu	His	Met	Leu	Val

260	265	270
Glu Thr Ala Gln Glu Arg Asn Glu Thr Leu Phe Pro Ala Leu Ile Tyr 275	280	285
Ser Ser Thr Met Val Trp Leu Val Asn Met Ala Glu Gly Asp Pro Glu 290	295	300
Ala Gln Arg Arg Val Ser Lys Asn Ser Lys His Asn Ala Glu Ser Thr 305	310	315
Glu Arg Glu Ser Gln Asp Thr Val Ala Glu Asn Asp Asp Gly Gly Phe 325	330	335
Ser Glu Glu Trp Glu Ala Gln Arg Asp Ser His Leu Gly Pro His Arg 340	345	350
Ser Thr Pro Glu Ser Arg Ala Ala Val Gln Glu Leu Ser Ser Ser Ile 355	360	365
Leu Ala Gly Glu Asp Pro Glu Glu Arg Gly Val Lys Leu Gly Leu Gly 370	375	380
Asp Phe Ile Phe Tyr Ser Val Leu Val Gly Lys Ala Ser Ala Thr Ala 385	390	395
Ser Gly Asp Trp Asn Thr Thr Ile Ala Cys Phe Val Ala Ile Leu Ile 405	410	415
Gly Leu Cys Leu Thr Leu Leu Leu Leu Ala Ile Phe Lys Lys Ala Leu 420	425	430
Pro Ala Leu Pro Ile Ser Ile Thr Phe Gly Leu Val Phe Tyr Phe Ala 435	440	445
Thr Asp Tyr Leu Val Gln Pro Phe Met Asp Gln Leu Ala Phe His Gln 450	455	460
Phe Tyr Ile 465		